What is claimed is:

1. A method for identifying a gene that modulates subcellular localization of a protein, said method comprising:

a) contacting a haploid or hypodiploid cell which expresses said protein with an insertional mutagen under conditions suitable to produce modified haploid or hypodiploid cell(s),

b) detecting a change in the subcellular localization of the protein as a result of the insertional mutagen; and

c) identifying, in those modified haploid or hypodiploid cells in which a change in the subcellular localization of the protein is detected, the gene into which the insertional mutagen is inserted, thereby identifying the gene that modulates subcellular localization of the protein.

2. A method for identifying a gene that modulates subcellular localization of a protein, said method comprising:

a) contacting a haploid or hypodiploid cell which expresses said protein with an insertional mutagen under conditions suitable to produce modified haploid or hypodiploid cell(s),

b) selecting those modified haploid or hypodiploid cells which reveal a change in the subcellular localization of the protein; and

c) identifying, in the modified haploid or hypodiploid cells selected in step (b), the gene into which the insertional mutagen is inserted, thereby identifying the gene that modulates subcellular localization of the protein.

3. A method for identifying a gene that modulates subcellular localization of a protein, said method comprising:

a) selecting modified haploid or hypodiploid cell(s) which express said protein and which reveal a change in the subcellular localization of the protein upon contacting with an insertional mutagen, and

b) identifying, in the modified haploid or hypodiploid cells selected in step (a), the gene into which the insertional mutagen is inserted, thereby identifying the gene that modulates subcellular localization of the protein.

4. A method for identifying a gene that modulates subcellular localization of a protein, said method comprising:

a) contacting a haploid or hypodiploid cell which expresses said protein with an insertional mutagen under conditions suitable to produce modified haploid or hypodiploid cell(s); and

b) identifying, in those modified haploid or hypodiploid cells in which a change in the subcellular localization of the protein occurs, the gene into which the insertional mutagen is inserted, thereby identifying the gene that modulates subcellular localization of the protein.

5. A method for identifying a gene that modulates subcellular localization of a protein, said method comprising identifying, in those modified haploid or hypodiploid cells which reveal a change in the subcellular localization of the protein upon introduction of an insertional mutagen thereto, the gene into which the insertional mutagen is inserted, thereby identifying the gene that modulates subcellular localization of the protein.

6. A method for identifying a gene that modulates cell morphology, said method comprising identifying, in those modified haploid or hypodiploid cells which reveal a change in the cell morphology upon introduction of an insertional mutagen thereto, the gene into which the insertional mutagen is inserted, thereby identifying the gene that modulates cell morphology.

7. A method for determining the enzymatic cascade of genes responsible for a protein modification of interest, said method comprising:

randomly mutagenizing a haploid or hypodiploid cell, optionally containing one or more stably expressed marker gene(s), with a mutagenic element,

selecting/detecting those cell lines that harbor the mutagenic element, and optionally one or more stably expressed marker gene(s), and

identifying, in the modified haploid or hypodiploid cells selected/detected above, a change in phenotype, thereby identifying a gene in the enzymatic cascade of interest.

8. A method for determining the enzymatic cascade of genes responsible for a protein modification of interest, said method comprising:

selecting/detecting those haploid or hypodiploid cells, optionally containing one or more stably expressed marker gene(s), that harbor a mutagenic element, and optionally one or more stably expressed marker gene(s) as a result of being randomly mutagenized with a mutagenic element, and

identifying, in the modified haploid or hypodiploid cells selected/detected above, a change in phenotype, thereby identifying a gene in the enzymatic cascade of interest.

9. A method for determining the enzymatic cascade of genes responsible for a protein modification of interest, said method comprising identifying a change in phenotype in modified haploid or hypodiploid cells prepared by randomly mutagenizing a haploid or hypodiploid cell, optionally containing one or more stably expressed marker gene(s), with a mutagenic element, thereby identifying a gene in the enzymatic cascade of interest.

10. A stable, haploid or hypodiploid line expressing a detectable marker, operably associated with a substrate for a reaction of interest.

11. A line according to claim 10 wherein said detectable marker is a fluorophore, a chromophore or a chromogenic substrate.

12. A line according to claim 10 wherein said detectable marker is a fluorophore.

13. A line according to claim 12 wherein said fluorophore is Green Fluorescent Protein (GFP).

14. A line according to claim 10 wherein said reaction of interest is palmitoylation.

15. A line according to claim 14 wherein the substrate is a short peptide.

16. A line according to claim 15 wherein said short peptide substrate is an S-palmitoylation substrate.

17. A line according to claim 10 wherein said reaction of interest is prenylation.

18. A line according to claim 10 wherein said reaction of interest is acylation.

19. A line according to claim 10 wherein said reaction of interest is regulation of transcription, the action of steroids and steroid-like compounds, neuroregeneration and spinal cord repair, cell cycle regulation, stem cells and neuronal stem cells, cell migration, filopodia, GPCR-related signaling, phosphorylation, contact-inhibition of cell growth, tumorigenesis, identification of the molecular targets of drugs with unknown mechanism(s) of action, and any signaling pathway or cellular process in which a unique morphological metric can be tied (either directly or indirectly) to that process.